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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Tue Jun 12 14:01:41 EDT 2007

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Application No: 10565997

Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-11 20:01:14.848

Finished: 2007-06-11 20:01:16.379

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 531 ms

Total Warnings: 32

Total Errors: 0

No. of SeqIDs Defined: 52

Actual SeqID Count: 52

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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
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Input Set:

Output Set:

Started: 2007-06-11 20:01:14.848
Finished: 2007-06-11 20:01:16.379
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 531 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 52
Actual SeqID Count: 52

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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 MANABE, ICHIRO
 ISHIHARA, ATSUSHI
 TOTTORI, TSUNEAKI

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<150> PCT/JP04/11223

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<150> JP 2003-202863

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                                     1

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Arg Val Leu Thr Met Ser Ala Arg Leu Gly Pro Leu Pro Gln Pro Pro
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Ala Ala Gln Ala Glu Pro Val Phe Ala Gln Leu Lys Pro Val Leu Gly
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gct gcg aac ccg gcc cgc gac gcg gcg ctc ttc tcc gga gac gat ctg      319
Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Ser Gly Asp Asp Leu
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Lys His Ala His His His Pro Pro Ala Pro Pro Pro Ala Ala Gly Pro	
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cga ctg ccc tcg gag gag ctg gtc cag aca aga tgt gaa atg gag aag	415
Arg Leu Pro Ser Glu Glu Leu Val Gln Thr Arg Cys Glu Met Glu Lys	
70 75 80	
tat ctg acc cct cag ctc cct cca gtt ccg ata att tca gag cat aaa	463
Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Ser Glu His Lys	
85 90 95	
aag tat aga cga gac agt gcc tca gtg gta gac cag ttc ttc act gac	511
Lys Tyr Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp	
100 105 110 115	
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Thr Glu Gly Ile Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp	
120 125 130	
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Ile Thr His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val	
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Thr Gln Ile Lys Thr Glu Pro Val Thr Ile Phe Ser His Gln Ser Glu	
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Ser Thr Ala Pro Pro Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu	
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Phe Thr Ser Ile Phe Ser Ser His Gln Thr Thr Ala Pro Pro Gln Glu	
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Val Asn Asn Ile Phe Ile Lys Gln Glu Leu Pro Ile Pro Asp Leu His	
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Leu Ser Val Pro Ser Gln Gln Gly His Leu Tyr Gln Leu Leu Asn Thr	
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Pro Asp Leu Asp Met Pro Ser Ser Thr Asn Gln Thr Ala Val Met Asp	
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Thr Leu Asn Val Ser Met Ala Gly Leu Asn Pro His Pro Ser Ala Val	
245 250 255	
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Pro Gln Thr Ser Met Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr	
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Ser Pro Thr Leu Pro Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp	
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Leu Glu Lys Arg Arg Ile His Phe Cys Asp Tyr Asn Gly Cys Thr Lys	
360 365 370	
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Val Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr	
375 380 385	
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Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala	
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Lys Pro Phe Gln Cys Met Val Cys Gln Arg Ser Phe Ser Arg Ser Asp	
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cgaccaagc cagcgtgggc gaggtgggaa gtgcgccga cccgcgctg gagctgcgcc 300

cccgagtgcc c atg gct aca agg gtg ctg agc atg agc gcc cgc ctg gga 350

Met Ala Thr Arg Val Leu Ser Met Ser Ala Arg Leu Gly

1

5

10

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15

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Leu Lys Pro Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu

30

35

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ttc ccc gcc gag gag ctg aag cac gcg cac cac cgc ccg cag gcg cag 494